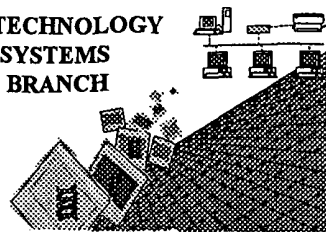BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____10|076,674_____

Source: _____O\PE_____

Date Processed by STIC: _____03|04|02_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
 http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

OIPE

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/076,674

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
    Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
    Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
    "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
    (OLD RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
    (NEW RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
    (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
    Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
    "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13__✓__Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

Does Not Comply   OIPE
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 03/04/2002
PATENT APPLICATION: US/10/076,674   TIME: 14:59:39

Input Set : A:\1151-4172.ST25.txt
Output Set: N:\CRF3\03042002\J076674.raw

```
     3 <110> APPLICANT: Sokoll, Kenneth K.
     5 <120> TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
     7 <130> FILE REFERENCE: Immunogen Delivery System
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/076,674
C--> 9 <141> CURRENT FILING DATE: 2002-02-14
     9 <160> NUMBER OF SEQ ID NOS: 11
    11 <170> SOFTWARE: PatentIn version 3.1
    13 <210> SEQ ID NO: 1
    14 <211> LENGTH: 32
    15 <212> TYPE: DNA
    16 <213> ORGANISM: Artificial Sequence
    18 <220> FEATURE:
    19 <223> OTHER INFORMATION: synthetic oligonucleotide
    21 <400> SEQUENCE: 1
    22 tcgtcgtttt gtcgttttgt cgttttgtcg tt                          32
    25 <210> SEQ ID NO: 2
    26 <211> LENGTH: 25
    27 <212> TYPE: DNA
    28 <213> ORGANISM: Artificial Sequence
    30 <220> FEATURE:
    31 <223> OTHER INFORMATION: synthetic oligonucleotide
    33 <220> FEATURE:
    34 <221> NAME/KEY: misc_feature
    35 <222> LOCATION: (1)..(1)
    36 <223> OTHER INFORMATION: n indicates phosphorothioate group
    39 <400> SEQUENCE: 2
W--> 40 ntcgtcgttt tgtcgttttg tcgtt                                  25
    43 <210> SEQ ID NO: 3
    44 <211> LENGTH: 24
    45 <212> TYPE: DNA
    46 <213> ORGANISM: Artificial Sequence
    48 <220> FEATURE:
    49 <223> OTHER INFORMATION: synthetic oligonucleotide
    51 <400> SEQUENCE: 3
    52 tcgtcgtttt gtcgttttgt cgtt                                   24
    55 <210> SEQ ID NO: 4
    56 <211> LENGTH: 50
    57 <212> TYPE: PRT
    58 <213> ORGANISM: Human
    60 <220> FEATURE:
    61 <221> NAME/KEY: misc_feature
    62 <222> LOCATION: (20)..(20)
    63 <223> OTHER INFORMATION: Xaa indicates epsilon-Lys
```

See error summary sheet item 13

n commonly represent a single nucleotide

```
                    RAW SEQUENCE LISTING              DATE: 03/04/2002
                    PATENT APPLICATION:  US/10/076,674  TIME: 14:59:40

                    Input Set : A:\1151-4172.ST25.txt
                    Output Set: N:\CRF3\03042002\J076674.raw

       66 <400> SEQUENCE: 4
       68 Ile Ser Ile Thr Glu Ile Lys Gly Val Ile Val His Arg Ile Glu Thr
       69 1               5                   10                  15
W--> 72 Ile Leu Phe Xaa Cys Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
       73              20                  25                  30
       76 Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
       77           35                  40                  45
       80 Asn Cys
       81     50
       84 <210> SEQ ID NO: 5
       85 <211> LENGTH: 50
       86 <212> TYPE: PRT
       87 <213> ORGANISM: Human
       89 <220> FEATURE:
       90 <221> NAME/KEY: misc_feature
       91 <222> LOCATION: (20)..(20)
       92 <223> OTHER INFORMATION: Xaa indicates epsilon-Lys
       95 <400> SEQUENCE: 5
       97 Lys Lys Lys Thr Asp Arg Val Ile Glu Val Leu Gln Arg Ala Gly Arg
       98 1               5                   10                  15
W--> 101 Ala Ile Leu Xaa Cys Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
       102             20                  25                  30
       105 Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
       106          35                  40                  45
       109 Asn Cys
       110     50
       113 <210> SEQ ID NO: 6
       114 <211> LENGTH: 31
       115 <212> TYPE: PRT
       116 <213> ORGANISM: Human
       118 <220> FEATURE:
       119 <221> NAME/KEY: misc_feature
       120 <222> LOCATION: (20)..(20)
       121 <223> OTHER INFORMATION: Xaa indicates epsilon-Lys
       124 <400> SEQUENCE: 6
       126 Ile Ser Ile Thr Glu Ile Lys Gly Val Ile Val His Arg Ile Glu Thr
       127 1               5                   10                  15
W--> 130 Ile Leu Phe Xaa Cys His Ala Ser Ile Tyr Asp Phe Gly Ser Cys
       131             20                  25                  30
       134 <210> SEQ ID NO: 7
       135 <211> LENGTH: 27
       136 <212> TYPE: PRT
       137 <213> ORGANISM: Human
       139 <400> SEQUENCE: 7
       141 Lys Lys Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
       142 1               5                   10                  15
       145 Leu Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
       146          20                  25
       149 <210> SEQ ID NO: 8
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```
150 <211> LENGTH: 45
151 <212> TYPE: PRT
152 <213> ORGANISM: Human
154 <400> SEQUENCE: 8
156 Thr Ala Lys Ser Lys Lys Phe Pro Ser Tyr Thr Ala Thr Tyr Gln Phe
157 1               5                   10                  15
160 Gly Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
161             20                  25                  30
164 Glu Gly Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
165             35                  40                  45
168 <210> SEQ ID NO: 9
169 <211> LENGTH: 45
170 <212> TYPE: PRT
171 <213> ORGANISM: Human
173 <400> SEQUENCE: 9
175 Thr Ala Lys Ser Lys Lys Phe Pro Ser Tyr Thr Ala Thr Tyr Gln Phe
176 1               5                   10                  15
179 Gly Gly Leu Ser Glu Ile Lys Gly Val Ile Val His Arg Leu Glu Gly
180             20                  25                  30
183 Val Gly Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
184             35                  40                  45
187 <210> SEQ ID NO: 10
188 <211> LENGTH: 44
189 <212> TYPE: PRT
190 <213> ORGANISM: Human
192 <220> FEATURE:
193 <221> NAME/KEY: misc_feature
194 <222> LOCATION: (19)..(19)
195 <223> OTHER INFORMATION: Xaa indicates epsilon-Lys
198 <400> SEQUENCE: 10
200 Lys Lys Lys Ile Ile Thr Ile Thr Arg Ile Ile Thr Ile Ile Thr Thr
201 1               5                   10                  15
W--> 204 Ile Asp Xaa Cys Gly Glu Thr Tyr Gln Ser Arg Val Thr His Pro His
205             20                  25                  30
208 Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Cys
209             35                  40
212 <210> SEQ ID NO: 11
213 <211> LENGTH: 45
214 <212> TYPE: PRT
215 <213> ORGANISM: Human
217 <220> FEATURE:
218 <221> NAME/KEY: misc_feature
219 <222> LOCATION: (20)..(20)
220 <223> OTHER INFORMATION: Xaa indicates epsilon-Lys
223 <400> SEQUENCE: 11
225 Ile Ser Ile Thr Glu Ile Lys Gly Val Ile Val His Arg Ile Glu Thr
226 1               5                   10                  15
W--> 229 Ile Leu Phe Xaa Cys Gly Glu Thr Tyr Gln Ser Arg Val Thr His Pro
230             20                  25                  30
```

RAW SEQUENCE LISTING   DATE: 03/04/2002
PATENT APPLICATION: US/10/076,674   TIME: 14:59:40

Input Set : A:\1151-4172.ST25.txt
Output Set: N:\CRF3\03042002\J076674.raw

233 His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Cys
234   35   40   45

VERIFICATION SUMMARY   DATE: 03/04/2002
PATENT APPLICATION: US/10/076,674   TIME: 14:59:41

Input Set : **A:\1151-4172.ST25.txt**
Output Set: **N:\CRF3\03042002\J076674.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11